



## SEQUENCE LISTING

&lt;110&gt; ITO, Kikukatsu

&lt;120&gt; Plant Thermogenic Genes and Proteins

&lt;130&gt; 2001-1838A/LC/00653

&lt;140&gt; 10/009,962

&lt;141&gt; 2002-01-23

&lt;150&gt; PCT/JP00/03806

&lt;151&gt; 2000-06-12

&lt;150&gt; JP11-167439

&lt;151&gt; 1999-06-14

&lt;160&gt; 12

&lt;170&gt; PatentIn Ver. 2.0

&lt;210&gt; 1

&lt;211&gt; 1525

&lt;212&gt; DNA

&lt;213&gt; Symplocarpus foetidus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (280)..(1188)

&lt;221&gt; poly A site

&lt;221&gt; (1271)..(1276)

&lt;300&gt;

&lt;301&gt; Ito, K.

&lt;302&gt; Isolation of two distinct cold-inducible cDNAs encoding plant uncoupling proteins from the

spadix of skunk cabbage (Symplocarpus foetidus)

&lt;303&gt; Plant Sci.

&lt;304&gt; 149

&lt;305&gt; 2

&lt;306&gt; 167-173

&lt;307&gt; Dec-1999

&lt;308&gt; GenBank AB024733

&lt;309&gt; 2000-02-25

&lt;400&gt; 1

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tcctctctac ataaacccta accacccat cctctcctcc cgcttccgac caccctgcat 240

tctactggga gcccatttga tcgagggttc cggcgagg atg ggc gat cac ggc 294

Met Gly Asp His Gly

1 5

ccg agg acc gag atc tcg ttt gcc ggc agt tcg cga gca gca ttc gcc 342

Pro Arg Thr Glu Ile Ser Phe Ala Gly Ser Ser Arg Ala Ala Phe Ala

10 15 20

gct tgc ttc gcc gag ctt tgc acg att ccg ttg gac act gct aaa gtt 390

Ala Cys Phe Ala Glu Leu Cys Thr Ile Pro Leu Asp Thr Ala Lys Val			
25	30	35	
agg ctt caa ctc caa aag aaa gca gta aca ggt gat gtg gtg gct ttg			438
Arg Leu Gln Leu Gln Lys Lys Ala Val Thr Gly Asp Val Val Ala Leu			
40	45	50	
cca aaa tac agg gga atg ttg ggc act gtt gcc act att gcc agg gag			486
Pro Lys Tyr Arg Gly Met Leu Gly Thr Val Ala Thr Ile Ala Arg Glu			
55	60	65	
gaa ggt ttg tcg gca ctc tgg aaa gga att gta ccc ggt ttg cat cgt			534
Glu Gly Leu Ser Ala Leu Trp Lys Gly Ile Val Pro Gly Leu His Arg			
70	75	80	85
caa tgc ctc ttt gga ggg cta cga att ggg ttg tat gaa cca gtt aag			582
Gln Cys Leu Phe Gly Gly Leu Arg Ile Gly Leu Tyr Glu Pro Val Lys			
90	95	100	
tcc ttt tat gtt gga gat aac ttt gtt gga gat att cct tta tcc aag			630
Ser Phe Tyr Val Gly Asp Asn Phe Val Gly Asp Ile Pro Leu Ser Lys			
105	110	115	
aaa ata ctt gct ggg ctt aca aca ggt gca tta gca att ata gtt gca			678
Lys Ile Leu Ala Gly Leu Thr Thr Gly Ala Leu Ala Ile Ile Val Ala			
120	125	130	
aat ccc act gac ctt gtt aaa gtt cga ctt caa tct gaa ggt aaa ctc			726
Asn Pro Thr Asp Leu Val Lys Val Arg Leu Gln Ser Glu Gly Lys Leu			
135	140	145	
ccc cct ggg gta ccg aga cgt tat tca ggg gcg cta aat gct tat tca			774
Pro Pro Gly Val Pro Arg Arg Tyr Ser Gly Ala Leu Asn Ala Tyr Ser			
150	155	160	165
acc ata gtc aaa aag gaa gga ctt ggt gct ctg tgg act ggg ctt ggt			822
Thr Ile Val Lys Lys Glu Gly Leu Gly Ala Leu Trp Thr Gly Leu Gly			
170	175	180	
cct aat att gcc cgc aat gct att ata aat gct gct gaa ttg gcc agt			870
Pro Asn Ile Ala Arg Asn Ala Ile Ile Asn Ala Ala Glu Leu Ala Ser			
185	190	195	
tat gat caa gtg aaa cag aca atc tta aaa tta cca gga ttc tca gat			918
Tyr Asp Gln Val Lys Gln Thr Ile Leu Lys Leu Pro Gly Phe Ser Asp			
200	205	210	
aat att ttt act cat att tta gcc ggt ctg ggg gca ggt ttt ttt gcc			966
Asn Ile Phe Thr His Ile Leu Ala Gly Leu Gly Ala Gly Phe Phe Ala			
215	220	225	
gtc tgt atc ggt tct cct gtt gat gtg atg aag tct aga atg atg gga			1014
Val Cys Ile Gly Ser Pro Val Asp Val Met Lys Ser Arg Met Met Gly			
230	235	240	245
gat tca gcc tac aaa agc aca ttt gat tgt ttc atc aag aca ttg aaa			1062
Asp Ser Ala Tyr Lys Ser Thr Phe Asp Cys Phe Ile Lys Thr Leu Lys			
250	255	260	
aat gat ggg ctt ctt gct ttt tac aag ggg ttt atc cca aac ttt ggt			1110
Asn Asp Gly Leu Leu Ala Phe Tyr Lys Gly Phe Ile Pro Asn Phe Gly			
265	270	275	
cgg tta gga tcg tgg aat gtg atc atg ttt ttg acc ttg gag cag gtc			1158
Arg Leu Gly Ser Trp Asn Val Ile Met Phe Leu Thr Leu Glu Gln Val			
280	285	290	
aag aag ttt ttc atc aaa gag gtg cca aat taatacatgg aactcggata			1208
Lys Lys Phe Phe Ile Lys Glu Val Pro Asn			
295	300		
ggagtagaaaa gaaagggttt ttgtggatt ttctctaccg gtgtggatcc tggcagaga			1268
caaataaattc ttccctgactg ctcagatgtg tacctttttt atgaatggtt cttttcttat			1328
agaggacaga gaaaagaaaa aaaaaatcat tgtcattac tctttttccc catttctgct			1388
gctaattctt gtaggagaag aaaagtctta cattgagtga taacgttgtt ctctgcatcc			1448

attattttc agagatacta tttgacacat gaaaagtaat gcacatcagg tttttttaa 1508  
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<211> 303  
<212> PRT  
<213> Symplocarpus foetidus

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20 25 30  
Asp Thr Ala Lys Val Arg Leu Gln Leu Gln Lys Lys Ala Val Thr Gly  
35 40 45  
Asp Val Val Ala Leu Pro Lys Tyr Arg Gly Met Leu Gly Thr Val Ala  
50 55 60  
Thr Ile Ala Arg Glu Glu Gly Leu Ser Ala Leu Trp Lys Gly Ile Val  
65 70 75 80  
Pro Gly Leu His Arg Gln Cys Leu Phe Gly Gly Leu Arg Ile Gly Leu  
85 90 95  
Tyr Glu Pro Val Lys Ser Phe Tyr Val Gly Asp Asn Phe Val Gly Asp  
100 105 110  
Ile Pro Leu Ser Lys Lys Ile Leu Ala Gly Leu Thr Thr Gly Ala Leu  
115 120 125  
Ala Ile Ile Val Ala Asn Pro Thr Asp Leu Val Lys Val Arg Leu Gln  
130 135 140  
Ser Glu Gly Lys Leu Pro Pro Gly Val Pro Arg Arg Tyr Ser Gly Ala  
145 150 155 160  
Leu Asn Ala Tyr Ser Thr Ile Val Lys Lys Glu Gly Leu Gly Ala Leu  
165 170 175  
Trp Thr Gly Leu Gly Pro Asn Ile Ala Arg Asn Ala Ile Ile Asn Ala  
180 185 190  
Ala Glu Leu Ala Ser Tyr Asp Gln Val Lys Gln Thr Ile Leu Lys Leu  
195 200 205  
Pro Gly Phe Ser Asp Asn Ile Phe Thr His Ile Leu Ala Gly Leu Gly  
210 215 220  
Ala Gly Phe Phe Ala Val Cys Ile Gly Ser Pro Val Asp Val Met Lys  
225 230 235 240  
Ser Arg Met Met Gly Asp Ser Ala Tyr Lys Ser Thr Phe Asp Cys Phe  
245 250 255  
Ile Lys Thr Leu Lys Asn Asp Gly Leu Leu Ala Phe Tyr Lys Gly Phe  
260 265 270  
Ile Pro Asn Phe Gly Arg Leu Gly Ser Trp Asn Val Ile Met Phe Leu  
275 280 285  
Thr Leu Glu Gln Val Lys Lys Phe Phe Ile Lys Glu Val Pro Asn  
290 295 300

<210> 3  
<211> 2991  
<212> DNA  
<213> Symplocarpus foetidus

<220>  
<221> CDS  
<222> (286)..(1089)  
<221> poly A site

<222> (1171)..(1176)  
<221> poly A site  
<222> (1243)..(1248)

<300>  
<301> Ito, K.  
<302> Isolation of two distinct cold-inducible cDNAs encoding plant uncoupling proteins from the spadix of skunk cabbage (*Symplocarpus foetidus*)  
<303> Plant Sci.  
<304> 149  
<305> 2  
<306> 167-173  
<307> Dec-1999  
<308> GenBank AB024734  
<309> 2000-02-25

<400> 3

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tttccgcgcc	aaacgccttc	cacccaatcc	ctccgttcc	cgaaatattc	cccttccctc	180	
cctttcttc	tctacataaaa	ccctaaccac	ccccatc	tcctcccgct	tccgaccacc	240	
ctgcattcta	ctggatccc	atttgc	cgagg	atg	ggc	gat	297
				Met	Gly	Asp	His
				1			
ggc ccg agg acc gag atc tcg ttt gcc ggc agt tcg cga gca gca ttc							345
Gly Pro Arg Thr Glu Ile Ser Phe Ala Gly Ser Ser Arg Ala Ala Phe							
5	10	15	20				
gcc gct tgc ttc gcc gag ctc tgt acg att ccg ttg gac act gct aaa							393
Ala Ala Cys Phe Ala Glu Leu Cys Thr Ile Pro Leu Asp Thr Ala Lys							
25	30	35					
gtt agg ctt cag ctc caa aag gca gta aca ggt gat gtg gtg gct							441
Val Arg Leu Gln Leu Gln Lys Lys Ala Val Thr Gly Asp Val Val Ala							
40	45	50					
ttg cca aaa tac agg gga atg ttg ggc act gtt gcc act att gcc agg							489
Leu Pro Lys Tyr Arg Gly Met Leu Gly Thr Val Ala Thr Ile Ala Arg							
55	60	65					
gag gaa ggt ttg tcg gca ctc tgg aaa gga att gta ccc ggt ttg cat							537
Glu Glu Gly Leu Ser Ala Leu Trp Lys Gly Ile Val Pro Gly Leu His							
70	75	80					
cgt caa tgc ctc ttt gga ggg cta cga att ggg ttg tat gaa cca gtt							585
Arg Gln Cys Leu Phe Gly Gly Leu Arg Ile Gly Leu Tyr Glu Pro Val							
85	90	95	100				
aag tcc ttt tat gtt gga gat aac ttt gtt gga gat att cct tta tcc							633
Lys Ser Phe Tyr Val Gly Asp Asn Phe Val Gly Asp Ile Pro Leu Ser							
105	110	115					
aag aaa ata ctt gct ggg ctt aca aca ggt gca tta gca att ata gtg							681
Lys Lys Ile Leu Ala Gly Leu Thr Thr Gly Ala Leu Ala Ile Ile Val							
120	125	130					
gca aat ccg act gac ctt gtt aaa gtt cga ctt caa tct gaa ggt aaa							729
Ala Asn Pro Thr Asp Leu Val Lys Val Arg Leu Gln Ser Glu Gly Lys							
135	140	145					
ctc ccc cct ggg gta cca aga cgt tat tca ggg gcg cta aat gct tat							777
Leu Pro Pro Gly Val Pro Arg Arg Tyr Ser Gly Ala Leu Asn Ala Tyr							
150	155	160					
tca acc ata gtc aaa aag gaa ctt ggt gct ctg tgg act ggg ctt							825
Ser Thr Ile Val Lys Lys Glu Gly Leu Gly Ala Leu Trp Thr Gly Leu							

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<211> 268  
<212> PRT  
<213> *Symplocarpus foetidus*

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Arg Ala Ala Phe Ala Ala Cys Phe Ala Glu Leu Cys Thr Ile Pro Leu  
20 25 30  
Asp Thr Ala Lys Val Arg Leu Gln Leu Gln Lys Lys Ala Val Thr Gly  
35 40 45  
Asp Val Val Ala Leu Pro Lys Tyr Arg Gly Met Leu Gly Thr Val Ala  
50 55 60  
Thr Ile Ala Arg Glu Glu Gly Leu Ser Ala Leu Trp Lys Gly Ile Val  
65 70 75 80  
Pro Gly Leu His Arg Gln Cys Leu Phe Gly Gly Leu Arg Ile Gly Leu  
85 90 95  
Tyr Glu Pro Val Lys Ser Phe Tyr Val Gly Asp Asn Phe Val Gly Asp  
100 105 110  
Ile Pro Leu Ser Lys Lys Ile Leu Ala Gly Leu Thr Thr Gly Ala Leu  
115 120 125  
Ala Ile Ile Val Ala Asn Pro Thr Asp Leu Val Lys Val Arg Leu Gln  
130 135 140  
Ser Glu Gly Lys Leu Pro Pro Gly Val Pro Arg Arg Tyr Ser Gly Ala  
145 150 155 160  
Leu Asn Ala Tyr Ser Thr Ile Val Lys Lys Glu Gly Leu Gly Ala Leu  
165 170 175  
Trp Thr Gly Leu Gly Pro Asn Ile Ala Arg Asn Ala Ile Asn Ala  
180 185 190  
Ala Glu Leu Ala Ser Tyr Asp Gln Val Lys Gln Met Lys Ser Arg Met  
195 200 205  
Met Gly Asp Ser Ala Tyr Lys Ser Thr Phe Asp Cys Phe Ile Lys Thr  
210 215 220  
Leu Lys Asn Asp Gly Pro Leu Ala Phe Tyr Lys Gly Phe Ile Pro Asn  
225 230 235 240  
Phe Gly Arg Leu Gly Ser Trp Asn Val Ile Met Phe Leu Thr Leu Glu  
245 250 255  
Gln Val Lys Lys Phe Phe Ile Lys Glu Val Pro Asn  
260 265

<210> 5  
<211> 306  
<212> PRT  
<213> Solanum Tuberosum

<400> 5  
Met Gly Gly Gly Asp His Gly Gly Lys Ser Asp Ile Ser Phe Ala Gly  
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Ile Phe Ala Ser Ser Ala Phe Ala Ala Cys Phe Ala Glu Ala Cys Thr  
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Leu Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Leu Gln Lys Lys Ala  
35 40 45  
Val Glu Gly Asp Gly Leu Ala Leu Pro Lys Tyr Arg Gly Leu Leu Gly  
50 55 60  
Thr Val Gly Thr Ile Ala Lys Glu Glu Gly Ile Ala Ser Leu Trp Lys  
65 70 75 80

Gly Ile Val Pro Gly Leu His Arg Gln Cys Ile Tyr Gly Gly Leu Arg  
85 90 95

Ile Gly Met Tyr Glu Pro Val Lys Asn Leu Tyr Val Gly Lys Asp His  
100 105 110

Val Gly Asp Val Pro Leu Ser Lys Lys Ile Leu Ala Ala Leu Thr Thr  
115 120 125

Gly Ala Leu Gly Ile Thr Ile Ala Asn Pro Thr Asp Leu Val Lys Val  
130 135 140

Arg Leu Gln Ala Glu Gly Lys Leu Pro Ala Gly Val Pro Arg Arg Tyr  
145 150 155 160

Ser Gly Ala Leu Asn Ala Tyr Ser Thr Ile Val Lys Gln Glu Gly Val  
165 170 175

Arg Ala Leu Trp Thr Gly Leu Gly Pro Asn Ile Gly Arg Asn Ala Ile  
180 185 190

Ile Asn Ala Ala Glu Leu Ala Ser Tyr Asp Gln Val Lys Glu Ala Val  
195 200 205

Leu Arg Ile Pro Gly Phe Thr Asp Asn Val Val Thr His Leu Ile Ala  
210 215 220

Gly Leu Gly Ala Gly Phe Phe Ala Val Cys Ile Gly Ser Pro Val Asp  
225 230 235 240

Val Val Lys Ser Arg Met Met Gly Asp Ser Ala Tyr Lys Asn Thr Leu  
245 250 255

Asp Cys Phe Val Lys Thr Leu Lys Asn Asp Gly Pro Leu Ala Phe Tyr  
260 265 270

Lys Gly Phe Ile Pro Asn Phe Gly Arg Leu Gly Ser Trp Asn Val Ile  
275 280 285

Met Phe Leu Thr Leu Glu Gln Ala Lys Lys Phe Val Lys Ser Leu Glu  
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Ser Pro  
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<213> Arabidopsis thaliana

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Asp Thr Ala Lys Val Arg Leu Gln Leu Gln Lys Ser Ala Phe Thr Leu  
35 40 45

Ala Gly Asp Val Thr Leu Pro Lys Tyr Arg Gly Leu Leu Gly Thr Val  
50 55 60

Gly Thr Ile Ala Arg Glu Glu Gly Leu Arg Ser Leu Trp Lys Gly Val  
65 70 75 80

Val Pro Gly Leu His Arg Gln Cys Leu Phe Gly Gly Leu Arg Ile Gly  
85 90 95

Met Tyr Glu Pro Val Lys Asn Leu Tyr Val Phe Thr Gly Lys Asp Phe  
100 105 110

Val Gly Asp Val Pro Leu Ser Lys Lys Ile Leu Ala Gly Leu Thr Thr  
115 120 125

Gly Ala Leu Gly Ile Met Val Ala Asn Pro Thr Asp Leu Val Lys Val  
130 135 140

Arg Leu Gln Ala Glu Gly Lys Leu Ala Ala Gly Ala Pro Arg Arg Tyr  
145 150 155 160

Ser Gly Ala Leu Asn Ala Tyr Phe Thr Ser Thr Ile Val Arg Gln Glu  
165 170 175

Gly Val Arg Ala Leu Trp Thr Val Leu Gly Pro Asn Val Ala Arg Asn  
180 185 190

Ala Ile Ile Asn Ala Ala Glu Leu Ala Ser Tyr Asp Gln Val Lys Glu  
195 200 205

Thr Ile Leu Lys Ile Pro Gly Phe Thr Asp Asn Val Val Thr His Ile  
210 215 220

Leu Ser Gly Leu Phe Thr Gly Ala Gly Phe Phe Ala Val Cys Ile Gly  
225 230 235 240

Ser Pro Val Asp Val Val Lys Ser Arg Met Met Gly Asp Ser Gly Ala  
245 250 255

Tyr Lys Gly Thr Ile Asp Cys Phe Val Lys Thr Leu Lys Ser Asp Gly  
260 265 270

Pro Met Ala Phe Tyr Lys Gly Phe Ile Pro Asn Phe Gly Arg Leu Gly  
275 280 285

Ser Phe Thr Trp Asn Val Ile Met Phe Leu Thr Leu Glu Gln Ala Lys  
290 295 300

Lys Tyr Val Arg Glu Leu Asp Ala Ser Lys Arg Asn  
305 310 315

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<211> 307

<212> PRT

<213> Homo sapiens

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Leu Phe Ser Ala Pro Ile Ala Ala Cys Leu Ala Asp Val Ile Thr Phe  
20 25 30

Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Val Gln Gly Glu Cys Pro  
35 40 45

Thr Ser Ser Val Ile Arg Tyr Lys Gly Val Leu Gly Thr Ile Thr Ala  
50 55 60

Val Val Lys Thr Glu Gly Arg Met Lys Leu Tyr Ser Gly Leu Pro Ala  
65 70 75 80

Gly Leu Gln Arg Gln Ile Ser Ser Ala Ser Leu Arg Ile Gly Leu Tyr  
85 90 95

Asp Thr Val Gln Glu Phe Leu Thr Ala Gly Lys Glu Thr Ala Pro Ser  
100 105 110

Leu Gly Ser Lys Ile Leu Ala Gly Leu Thr Thr Gly Gly Val Ala Val  
115 120 125

Phe Ile Gly Gln Pro Thr Glu Val Val Lys Val Arg Leu Gln Ala Gln  
130 135 140

Ser His Leu His Gly Ile Lys Pro Arg Tyr Thr Gly Thr Tyr Asn Ala  
145 150 155 160

Tyr Arg Ile Ile Ala Thr Thr Glu Gly Leu Thr Gly Leu Trp Lys Gly  
165 170 175

Thr Thr Pro Asn Leu Met Arg Ser Val Ile Ile Asn Cys Thr Glu Leu  
180 185 190

Val Thr Tyr Asp Leu Met Lys Glu Ala Phe Val Lys Asn Asn Ile Leu  
195 200 205

Ala Asp Asp Val Pro Cys His Leu Val Ser Ala Leu Ile Ala Gly Phe  
210 215 220

Cys Ala Thr Ala Met Ser Ser Pro Val Asp Val Val Lys Thr Arg His  
225 230 235 240

Ile Asn Ser Pro Pro Gly Gln Tyr Lys Ser Val Pro Asn Cys Ala Met  
245 250 255

Lys Val Phe Thr Asn Glu Gly Pro Thr Ala Phe Phe Lys Gly Leu Val  
260 265 270

Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val Ile Met Phe Val Cys  
275 280 285

Phe Glu Gln Leu Lys Arg Glu Leu Ser Lys Ser Arg Gln Thr Met Asp  
290 295 300

Cys Ala Thr  
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<212> PRT  
<213> Homo sapiens

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20 25 30

Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile Gln Gly Glu Ser Gln  
35 40 45

Gly Pro Val Arg Ala Thr Ala Ser Ala Gln Tyr Arg Gly Val Met Gly  
50 55 60

Thr Ile Leu Thr Met Val Arg Thr Glu Gly Pro Arg Ser Leu Tyr Asn  
65 70 75 80

Gly Leu Val Ala Gly Leu Gln Arg Gln Met Ser Phe Ala Ser Val Arg  
85 90 95

Ile Gly Leu Tyr Asp Ser Val Lys Gln Phe Tyr Thr Lys Gly Ser Glu  
100 105 110

His Ala Ser Ile Gly Ser Arg Leu Leu Ala Gly Ser Thr Thr Gly Ala  
115 120 125

Leu Ala Val Ala Val Ala Gln Pro Thr Asp Val Val Lys Val Arg Phe  
130 135 140

Gln Ala Gln Ala Arg Ala Gly Gly Arg Arg Tyr Gln Ser Thr Val  
145 150 155 160

Asn Ala Tyr Lys Thr Ile Ala Arg Glu Glu Gly Phe Arg Gly Leu Trp  
165 170 175

Lys Gly Thr Ser Pro Asn Val Ala Arg Asn Ala Ile Val Asn Cys Ala  
180 185 190

Glu Leu Val Thr Tyr Asp Leu Ile Lys Asp Ala Leu Leu Lys Ala Asn  
195 200 205

Leu Met Thr Asp Asp Leu Pro Cys His Phe Thr Ser Ala Phe Gly Ala  
210 215 220

Gly Phe Cys Thr Thr Val Ile Ala Ser Pro Val Asp Val Val Lys Thr  
225 230 235 240

Arg His Met Asn Ser Ala Leu Gly Gln Tyr Ser Ser Ala Gly His Cys  
245 250 255

Ala Leu Thr Met Leu Gln Lys Glu Gly Pro Arg Ala Phe Tyr Lys Gly  
260 265 270

Phe Met Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val Val Met Phe  
275 280 285

Val Thr Tyr Glu Gln Leu Lys Arg Ala Leu Met Ala Ala Cys Thr Ser  
290 295 300

Arg Glu Ala Pro Phe  
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20 25 30

Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile Gln Gly Glu Asn Gln  
35 40 45

Ala Val Gln Thr Ala Arg Leu Val Gln Tyr Arg Gly Val Leu Gly Thr  
50 55 60

Ile Leu Thr Met Val Arg Thr Glu Gly Pro Cys Ser Pro Tyr Asn Gly  
65 70 75 80

Leu Val Ala Gly Leu Gln Arg Gln Met Ser Phe Ala Ser Ile Arg Ile  
85 90 95

Gly Leu Tyr Asp Ser Val Lys Gln Val Tyr Thr Pro Lys Gly Ala Asp  
100 105 110

Asn Ser Ser Leu Thr Thr Arg Ile Leu Ala Gly Cys Thr Thr Gly Ala  
115 120 125

Met Ala Val Thr Cys Ala Gln Pro Thr Asp Val Val Lys Val Arg Phe  
130 135 140

Gln Ala Ser Ile His Leu Gly Pro Ser Arg Ser Asp Arg Lys Tyr Ser  
145 150 155 160

Gly Thr Met Asp Ala Tyr Arg Thr Ile Ala Arg Glu Glu Gly Val Arg  
165 170 175

Gly Leu Trp Lys Gly Thr Leu Pro Asn Ile Met Arg Asn Ala Ile Val  
180 185 190

Asn Cys Ala Glu Val Val Thr Tyr Asp Ile Leu Lys Glu Lys Leu Leu  
195 200 205

Asp Tyr His Leu Leu Thr Asp Asn Phe Pro Cys His Phe Val Ser Ala  
210 215 220

Phe Gly Ala Gly Phe Cys Ala Thr Val Val Ala Ser Pro Val Asp Val  
225 230 235 240

Val Lys Thr Arg His Met Asn Ser Pro Pro Gly Gln Tyr Phe Ser Pro  
245 250 255

Leu Asp Cys Met Ile Lys Met Val Ala Gln Glu Gly Pro Thr Ala Phe  
260 265 270

Tyr Lys Gly Phe Thr Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val  
275 280 285

Val Met Phe Val Thr Tyr Glu Gln Leu Lys Arg Ala Leu Met Lys Val  
290 295 300

Gln Met Leu Arg Glu Ser Pro Phe  
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA Primer

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<210> 11

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Conserved UCP Peptide Fragment

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1 5 10 15

Ala Arg

<210> 12

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Conserved UCP Peptide Fragment

<400> 12

Ala Cys Trp Thr Thr Cys Cys Ala Ile Ser Tyr Ile Cys Cys Ile Ala  
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Trp Ile Cys